**Supplementary Text:**

Additionally all the code used for the analysis and figure generation have been deposited at github. (<https://github.com/rintukutum/fdr-celiac-manuscript>)

Composite figures were generated using inkscape and corresponding .svg files have been also uploaded in the github repository. (<https://github.com/rintukutum/fdr-celiac-manuscript/tree/master/figures/svg>)

**Supplementary Tables**

All the supplementary tables (excel and pdf) were uploaded at zenodo ([https://zenodo.org](https://zenodo.org/)).

**1. Table-S1-Differentially-expressed-genes.xlsx**

List of differentially expressed probes(genes) based on ajusted-pvalue <= 0.05 and |log2(FC)| >= 1. <http://doi.org/10.5281/zenodo.1296053>(need to change)

**2. Table-S2-data-for-FigureS1.xlsx**

List of genes up-regulated and down-regulated in FDR and CeD. <http://doi.org/10.5281/zenodo.1296055>

**3a. Table-S3a-GO-pval-0.05-DE.xlsx**

Gene ontology enrichment results for differentially expressed genes among FDR, CeD and Control.

<http://doi.org/10.5281/zenodo.1296059>

**3b. Table-S3b-MsigDB\_Consistently\_down\_in\_FDR.xlsx**

MSigDB enrichment analysis based on genes which are down-regualted consistently in FDR.

<http://doi.org/10.5281/zenodo.1296061>

**3c. Table-S3c-Reactome-Down-in-FDR.xlsx**

Reactome pathway enrichment for down in FDR based on adjusted-pvalue <= 0.05 and without log2(FC) criteria. <http://doi.org/10.5281/zenodo.1296063>

**4a. Table-S4a-pattern-analysis.xlsx**

List of probes/genes with their gene expression pattern among CeD, FDR and Control.

<http://doi.org/10.5281/zenodo.1296065>

**4b. Table-S4b-GO\_pattern.xlsx**

Gene ontology enrichment analysis based on genes for each expression pattern observed among CeD, FDR and Control. <http://doi.org/10.5281/zenodo.1296067>

**5. Table-S5-pseudogenes-DE-clsuter-ID-annotations.xls**

List of pseudogenes differentially expressed among CeD, FDR and Control. <http://doi.org/10.5281/zenodo.1296069>

**6. Table-S6-TranscriptionFactors-YY1-KLFs-NFKB-inhibitors.xlsx**

Detail information of p-value, log2(FC), adjusted-pvalue etc. for selected tanscription factors.

<http://doi.org/10.5281/zenodo.1296071>

**7. Table-S7\_qPCR\_gene\_expression\_fold\_change.pdf**

Gene expression fold-change of study groups: Anti-tTG positive FDR, CeD, DC, Anti-tTG negative FDR. <http://doi.org/10.5281/zenodo.1296074>